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<120> Wasch- und Reinigungsmittel mit Hybrid-Alpha-Amylasen

<130> H 4714 PCT

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<150> DE 10138753.9-41
<151> 2001-08-07

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<170> PatentIn Ver. 2.1

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aat gac ggc caa cat tgg aag cgc ttg caa aac gac tcg gca tat ttg    96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
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gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga   144
Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
         35                  40                  45

acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta   192
Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
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ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa   240
Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65                  70                  75                  80

gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac   288
Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
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gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc   336
Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
            100                 105                 110

gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta   384
Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
        115                 120                 125

att tca gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg   432
Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro
    130                 135                 140
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ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt    480
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gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag    528
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
                165                170                175

ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac    576
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180                185                190

tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc    624
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
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gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa    672
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225                230                235                240

ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg    768
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
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ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac    816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
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tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt    864
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
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cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg    912
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290                295                300

agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg    960
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305                310                315                320

gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag    1008
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
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Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
                    450                     455                     460

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Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
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Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
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Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
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Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
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Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
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225                 230                 235                 240
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His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
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Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
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Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
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Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
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Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
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Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                   425                   430
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
        435                   440                   445
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                   455                   460
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Val Gln Arg
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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat      96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
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atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc     144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
         35                  40                  45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa     192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
     50                  55                  60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag     240
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gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat    336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg    384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt    432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
    130                 135                 140

gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga    480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160

gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt    528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac    576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
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tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc    624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
        195                 200                 205

gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca    672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
    210                 215                 220

tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt    720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg    768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
            245                 250                 255

ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac    816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
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cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg    912
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
    290                 295                 300

agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg    960
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa    1008
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
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ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac    288
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                85                  90                  95

gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat    336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg    384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
            115                 120                 125

gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt    432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
        130                 135                 140

gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga    480
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145                 150                 155                 160

gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt    528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac    576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
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tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc    624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
            195                 200                 205

gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca    672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
        210                 215                 220

tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt    720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg    768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245                 250                 255

ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac    816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
            260                 265                 270

tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt    864
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
            275                 280                 285

cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg    912
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
        290                 295                 300

agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg    960
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa   1008
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
            325                 330                 335
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tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg    1056
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            355                 360                 365

aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata    1152
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
            370                 375                 380

gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac    1200
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                 390                 395                 400

gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt gac    1248
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac gga ccc    1296
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

ggc gga tca aag cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca    1344
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
            435                 440                 445

tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga tct    1392
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
            450                 455                 460

gac ggc tgg gga gag ttt cat gta aac gat ggg tcc gtc tcc att tat    1440
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Ile Gly Ile Thr Ala Val Trp Ile Pro Ala Tyr Lys Gly Leu Ser
        35                  40                  45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
     50                  55                  60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65                  70                  75                  80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
            115                 120                 125
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Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
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Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180                 185                 190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
        195                 200                 205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
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Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
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Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
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His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
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Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
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Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
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Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
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Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
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Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                 390                 395                 400
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
                420                 425                 430
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
            435                 440                 445
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
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Val Gln Lys
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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30

atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc     144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
            35                  40                  45

caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag     192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60

ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag     240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
65                  70                  75                  80

ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac     288
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
                85                  90                  95

ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat     336
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
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gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca     384
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
            115                 120                 125

gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc     432
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
        130                 135                 140

ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga     480
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160

acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag ttt caa     528
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                165                 170                 175

gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat     576
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
            180                 185                 190

tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca     624
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
            195                 200                 205

gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac     672
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
        210                 215                 220

ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cgg     720
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225                 230                 235                 240

gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg     768
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
            245                 250                 255
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gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg    816
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
            260             265             270

aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat    864
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
        275             280             285

cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa    912
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290             295             300

ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca    960
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305             310             315             320

ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act   1008
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
            325             330             335

gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg   1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
            340             345             350

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Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
        355             360             ·365

gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg   1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370             375             380

atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat   1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385             390             395             400

ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg   1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
            405             410             415

gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg   1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420             425             430

gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat   1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
        435             440             445

gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc   1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450             455             460

tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa   1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
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aga tag                                                            1446
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H04714.txt

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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
            35                  40                  45
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65                 70                  75                  80
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
                85                  90                  95
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
        115                 120                 125
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
    130                 135                 140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                165                 170                 175
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
                180                 185                 190
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
            195                 200                 205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
    210                 215                 220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225                 230                 235                 240
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                245                 250                 255
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
            260                 265                 270
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
        275                 280                 285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290                 295                 300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305                 310                 315                 320
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
                325                 330                 335
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
            340                 345                 350
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
        355                 360                 365
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370                 375                 380
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385                 390                 395                 400
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405                 410                 415
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
        420                 425                 430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
    435                 440                 445
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Page 10

Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450   455   460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465   470   475   480
Arg

<210> 7
<211> 1446
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (AL76).

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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat   96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
             20   25   30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
         35   40   45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa   192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
     50   55   60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa gga gag   240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65   70   75   80

ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac   288
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
                 85   90   95

ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat   336
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
            100   105   110

gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca   384
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
            115   120   125

gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc   432
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
        130   135   140

ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga   480
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145   150   155   160

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acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag ttt caa    528
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
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gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat    576
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
                180                 185                 190

tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca    624
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
                195                 200                 205

gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac    672
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
    210                 215                 220

ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cgg    720
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225                 230                 235                 240

gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg    768
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                245                 250                 255

gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg    816
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
                260                 265                 270

aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat    864
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
                275                 280                 285

cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa    912
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290                 295                 300

ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca    960
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305                 310                 315                 320

ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act    1008
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
                325                 330                 335

gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg    1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
                340                 345                 350

gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa    1104
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
                355                 360                 365

gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg    1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370                 375                 380

atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat    1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385                 390                 395                 400

ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg    1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405                 410                 415
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gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg   1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420               425               430

gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat   1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
            435               440               445

gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc   1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450               455               460

tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa   1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465               470               475               480

aga tag                                                            1446
Arg
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<210> 8
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<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (AL76).

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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
            35                  40                  45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
65                  70                  75                  80
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
                85                  90                  95
Gly Asp Val Val Ile Asn His Lys Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
            115                 120                 125
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
        130                 135                 140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                165                 170                 175
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
            180                 185                 190
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
        195                 200                 205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
210                 215                 220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225                 230                 235                 240
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                245                 250                 255
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
                        Page 13
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            260                 265                 270
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
        275                 280                 285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290                 295                 300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305                 310                 315                 320
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
            325                 330                 335
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
        340                 345                 350
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
        355                 360                 365
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370                 375                 380
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385                 390                 395                 400
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
            405                 410                 415
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420                 425                 430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
        435                 440                 445
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450                 455             -   460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465                 470                 475                 480
Arg
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<210> 9
<211> 1446
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:Fusion der
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      amyloliquefaciens (AL112).

<220>
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<222> (1)..(1446)

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ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat    96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30


atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
        35                  40                  45


caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa   192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
    50                  55                  60


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                      85              90              95

     gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat   336
     Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
                 100             105             110

     gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca   384
     Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
                 115             120             125

     gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc   432
     Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
             130             135             140

     ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga   480
     Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
     145             150             155             160

     acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag ttt caa   528
     Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                     165             170             175

     gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat   576
     Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
                 180             185             190

     tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca   624
     Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
             195             200             205

     gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac   672
     Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
             210             215             220

     ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cgg   720
     Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
     225             230             235             240

     gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg   768
     Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                     245             250             255

     gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg   816
     Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
                 260             265             270

     aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat   864
     Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
                 275             280             285

     cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa   912
     Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
             290             295             300

     ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca   960
     Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
     305             310             315             320
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ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act    1008
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
            325                 330                 335

gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg    1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
            340                 345                 350

gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa    1104
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
            355                 360                 365

gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg    1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
            370                 375                 380

atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat    1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385                 390                 395                 400

ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg    1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405                 410                 415

gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg    1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420                 425                 430

gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat    1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
            435                 440                 445

gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc    1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
            450                 455                 460

tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa    1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465                 470                 475                 480

aga tag                                                             1446
Arg
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<210> 10
<211> 481
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (AL112).

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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
        35                  40                  45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65                  70                  75                  80
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Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
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            100                   105                   110
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
            115                   120                   125
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
    130                   135                   140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                   150                   155                   160
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                165                   170                   175
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            180                   185                   190
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
        195                   200                   205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
    210                   215                   220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225                   230                   235                   240
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                245                   250                   255
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
            260                   265                   270
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
    275                   280                   285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290                   295                   300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305                   310                   315                   320
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
                325                   330                   335
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
            340                   345                   350
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
            355                   360                   365
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370                   375                   380
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385                   390                   395                   400
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405                   410                   415
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
            420                   425                   430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
        435                   440                   445
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450                   455                   460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465                   470                   475                   480
Arg
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<220>
<221> CDS
<222> (1)..(1452)

<400> 11
gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac   48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1   5   10   15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat   96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20   25   30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
        35   40   45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa   192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
    50   55   60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag   240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65   70   75   80

ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac   288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85   90   95

gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat   336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100   105   110

gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg   384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
            115   120   125

gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt   432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
        130   135   140

gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga   480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145   150   155   160

gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt   528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165   170   175

ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac   576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180   185   190

tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc   624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
            195   200   205

gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca   672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
        210   215   220

tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt   720
                            Page 18

```
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225             230             235             240

ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg    768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245             250             255

ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac    816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
                260             265             270

tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt    864
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
            275             280             285

cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg    912
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
        290             295             300

agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg    960
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305             310             315             320

gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag   1008
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325             330             335

tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc   1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
                340             345             350

aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg   1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
            355             360             365

acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att   1152
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
        370             375             380

gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat   1200
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385             390             395             400

gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac   1248
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
                405             410             415

agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc   1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
                420             425             430

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca   1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
            435             440             445

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg   1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450             455             460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat   1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465             470             475             480
```

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gtt caa aga tag   1452
Val Gln Arg

<210> 12
<211> 483
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (AL256).

<400> 12
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1   5   10   15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
                20   25   30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
            35   40   45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
        50   55   60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65   70   75   80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85   90   95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100   105   110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115   120   125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
    130   135   140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145   150   155   160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165   170   175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180   185   190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
        195   200   205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
    210   215   220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225   230   235   240
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245   250   255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
            260   265   270
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
        275   280   285
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
    290   295   300
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305   310   315   320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325   330   335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340   345   350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355   360   365
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
    370   375   380
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385   390   395   400

```
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
            405             410                         415
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
                420                 425             430
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
            435             440             445
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                 455             460
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                 470             475                     480
Val Gln Arg
```

<210> 13
<211> 1452
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:Fusion der
     Alpha-Amylase-Gene von B. licheniformis und B.
     amyloliquefaciens (ALA34-84).

<220>
<221> CDS
<222> (1)..(1452)

<400> 13
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gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac    48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1               5                  10                  15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat    96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
                20                  25                  30

atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
            35                  40                  45

caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag   192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60

ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag   240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
65                  70                  75                  80

ctg caa tct gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac   288
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95

gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat   336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg   384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt   432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
```
Page 21

```
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga    480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145             150                 155                 160

gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt    528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac    576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180                 185                 190

tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc    624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
            195                 200                 205

gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca    672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210                 215                 220

tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt    720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg    768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245                 250                 255

ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac    816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
                260                 265                 270

tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt    864
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
            275                 280                 285

cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg    912
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
            290                 295                 300

agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg    960
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa    1008
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                 330                 335

tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg    1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg tac ggg    1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
            355                 360                 365

aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata    1152
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
370                 375                 380

gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac    1200
```

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```
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385             390             395             400

gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt gac    1248
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
            405             410             415

agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac gga ccc    1296
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420             425             430

ggc gga tca aag cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca    1344
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
            435             440             445

tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga tct    1392
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450             455             460

gac ggc tgg gga gag ttt cat gta aac gat ggg tcc gtc tcc att tat    1440
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465             470             475             480

gtt cag aaa taa                                                    1452
Val Gln Lys
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<210> 14
<211> 483
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (ALA34-84).

<400> 14
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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
  1           5                  10                  15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
            35                  40                  45
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
        50                  55                  60
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65                  70                  75                  80
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
            115                 120                 125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
        130                 135                 140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
                180                 185                 190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
            195                 200                 205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
```

H04714.txt

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        210                    215                    220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                    230                    235                    240
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245                    250                    255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
            260                    265                    270
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
        275                    280                    285
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
    290                    295                    300
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                    310                    315                    320
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                    330                    335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                    345                    350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                    360                    365
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                    375                    380
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                    390                    395                    400
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                    410                    415
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                    425                    430
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                    440                    445
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450                    455                    460
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                    470                    475                    480
Val Gln Lys
```

<210> 15
<211> 1458
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:Fusion der
     Alpha-Amylase-Gene von B. licheniformis und B.
     amyloliquefaciens (LAL19-433).

<220>
<221> CDS
<222> (1)..(1458)

<400> 15
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gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc   48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
  1               5                  10                  15

aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta   96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
             20                  25                  30

tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga  144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
         35                  40                  45
```

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ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta   192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
    50              55              60

gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa   240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65              70              75              80

tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa   288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
                85              90              95

gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca   336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
            100             105             110

gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa   384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
            115             120             125

act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg   432
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
    130             135             140

ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc   480
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145             150             155             160

gac gga gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag   528
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
                165             170             175

ttt cgt ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac   576
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
            180             185             190

ggc aac tat gac tat tta atg tat gct gat gtt gac tac gac cac cct   624
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
            195             200             205

gat gtc gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa   672
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
    210             215             220

ctg tca tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt   720
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
225             230             235             240

tca ttt ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa   768
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
                245             250             255

gaa atg ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc   816
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
            260             265             270

gaa aac tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt   864
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
            275             280             285

ccg ctt cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat   912
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr
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         290                    295                    300
gat atg agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa    960
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
305                 310                 315                 320

aag gcg gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca   1008
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
                325                 330                 335

ttg gaa tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt   1056
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
                340                 345                 350

att ttg aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg   1104
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
                355                 360                 365

tac ggg aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat   1152
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
        370                 375                 380

aat ata gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc   1200
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
385                 390                 395                 400

cag cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa   1248
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
                405                 410                 415

ggt gac agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac   1296
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
                420                 425                 430

gga ccc ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt   1344
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
                435                 440                 445

gag aca tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc   1392
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
        450                 455                 460

aat tcg gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca   1440
Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

att tat gtt caa aga tag                                            1458
Ile Tyr Val Gln Arg
                485
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<210> 16
<211> 485
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (LAL19-433).

<400> 16
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
  1               5                  10                  15
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
```

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                 20                          25                          30
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
        35                          40                          45
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
    50                          55                          60
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65                          70                          75                          80
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
                    85                          90                          95
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
            100                         105                         110
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
            115                         120                         125
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
        130                         135                         140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145                         150                         155                         160
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
                    165                         170                         175
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
            180                         185                         190
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
        195                         200                         205
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
    210                         215                         220
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
225                         230                         235                         240
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
                    245                         250                         255
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
            260                         265                         270
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
            275                         280                         285
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr
    290                         295                         300
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
305                         310                         315                         320
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
                    325                         330                         335
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
            340                         345                         350
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
            355                         360                         365
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
    370                         375                         380
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
385                         390                         395                         400
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
                    405                         410                         415
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
            420                         425                         430
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
        435                         440                         445
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
    450                         455                         460
Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
465                         470                         475                         480
Ile Tyr Val Gln Arg
            485
```

<210> 17

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<211> 1452
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (LAL19-153).

<220>
<221> CDS
<222> (1)..(1452)

<400> 17
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc      48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
  1               5                  10                  15

aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta      96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
             20                  25                  30

tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga     144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
         35                  40                  45

ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta     192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
     50                  55                  60

gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa     240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65                  70                  75                  80

tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa     288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
                 85                  90                  95

gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca     336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
            100                 105                 110

gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa     384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
            115                 120                 125

act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg     432
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
        130                 135                 140

ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tac cat ttt     480
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145                 150                 155                 160

gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag     528
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
                165                 170                 175

ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac     576
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180                 185                 190

tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc     624
                              Page 28
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Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
    195   200   205

gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa   672
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210   215   220

ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt   720
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225   230   235   240

ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg   768
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
                 245   250   255

ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac   816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
                 260   265   270

tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt   864
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
                 275   280   285

cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg   912
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
         290   295   300

agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg   960
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305   310   315   320

gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag   1008
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                 325   330   335

tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc   1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
                 340   345   350

aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg   1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
         355   360   365

acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att   1152
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370   375   380

gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat   1200
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385   390   395   400

gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac   1248
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
         405   410   415

agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc   1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
         420   425   430

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca   1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
         435   440   445

```
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg   1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450             455             460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat   1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465             470             475             480

gtt caa aga tag                                                    1452
Val Gln Arg
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<210> 18
<211> 483
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
      Alpha-Amylase-Gene von B. licheniformis und B.
      amyloliquefaciens (LAL19-153).

<400> 18

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Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1               5               10              15
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
            20              25              30
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
        35              40              45
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
    50              55              60
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65              70              75              80
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
            85              90              95
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
            100             105             110
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
    115             120             125
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
    130             135             140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145             150             155             160
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
            165             170             175
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180             185             190
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
    195             200             205
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210             215             220
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225             230             235             240
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
            245             250             255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
            260             265             270
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
    275             280             285
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290             295             300
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305             310             315             320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
            325             330             335
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Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
    370                 375                 380
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385                 390                 395                 400
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
            405                 410                 415
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
        435                 440                 445
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                 455                 460
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                 470                 475                 480
Val Gln Arg
```